REMARKS

Amendments

The Title has been amended to correspond with the claim preambles. If the Examiner prefers an alternative title, we authorize the Examiner to amend the title accordingly. The specification hyperlinks have been amended to place the URL between angle brackets (<>) as suggested. These amendments introduce no new matter.

35USC102(e): Claims 1-4, 6, 8-24.

Ford et al. (US Pat. No. 6,472,173) describes a G protein-coupled chemokine receptor clone obtained from a fetal liver-spleen cDNA library. Other aspects of the disclosure are receptor polypeptides encoded by this clone, vectors, transformed host cells and specific antibodies. The Action cites the following sections of Ford:

Section 6.11, entitled "Computer Readable Sequences" discloses that the nucleotide sequences of the invention can be recorded on computer readable media, such as floppy discs, magnetic tape, etc. (col.22, lines 38 - 58); that the sequence data may be recorded in a variety of data structures, including text files, Microsoft Word files, etc. (col.22, line 59 - col.23, line 9); and that computer software such as BLAST may be used to access and analyze the recorded sequence information (col.23, lines 10 - Col.24, line 17).

Section 6.12, entitled "Expression Modulating Sequences" discloses that regulatory elements (e.g. promoters) can be identified by their proximity to open reading frames, and that their activity can be confirmed using gene trap vectors expressed in host cells.

Section 6.14, entitled "Diagnostic Assays and Kits", discloses methods to detect the subject polynucleotides using a nucleic acid or antibody probe.

Section 6.16, entitled "Use of Nucleic Acids as Probes" describes how the polynucleotides can be used as probes in hybridization reactions to map chromosomes and to detect differences between genomic samples. The polynucleotides may also be used to produce polypeptides by recombinant DNA technology. Homologous sequences can be found in GenBank using a search alorgithm developed by ABI and incorporated into their INHERIT 670 Sequence Analysis System. Alternatively, BLAST can be used to search for local sequence alignments, and to search for related molecules within the libraries of the LIFESEQ database.

All our claims recite a computer-based system for creating a targeted collection of sequences from a dataset or a plurality of datasets of sequence identifiers corresponding to natural complex biopolymer sequences which may be linked to corresponding annotations (in one practical application, the targeted collection of sequences may be used to assemble cDNA sequences for a particular gene expression microarray). For example, the system of our representative claim 1 must provide all four of the following functions:

a) a search function which searches the annotations of the dataset (such as GenBank) according to a user-defined criterion (such as by keyword) and outputs a first subset of the dataset restricted by the criterion;

b) a redundancy reducing function which compares the first subset with a first database (such as UniGene) correlating the sequence identifiers of the first subset with syngeneic biopolymers and outputs a second subset of the dataset having reduced unique, natural complex biopolymer redundancy relative to the first subset;

c) a selection function which applies to the second subset a user-defined selection parameter (such as source, species or author) and outputs a third subset restricted relative to the second subset by the parameter; and

d) a tabulation function which creates and outputs the targeted collection of sequences in the form of a data table comprising, configurable by and sortable by the sequence identifiers of the third subset.

The only computer-based systems described by Ford et al. are the referenced search and alignment protocols, such as MacPattern, BLAST, and the search function embedded in INHERIT. These protocols do not go past the initial search function (step (a)) of our method: there is no provision in MacPattern, BLAST, etc., for reducing redundancy of the search results by mapping to a database correlating sequence identifiers with syngeneic biopolymers to generate a second dataset subset (step (b)); and hence, no provision for further processing the resultant second dataset subset, as required by steps (c) - (d). Note that analogous required steps for reducing redundancy of the initial search results by mapping to a database correlating sequence identifiers with syngeneic biopolymers are present in all of our claims (e.g. step (b) of claim 13, and step (a) of claims 14, 17, 18 and 20).

The cited col.24, lines 20-30 of Ford et al. relate to identifying EMF sequences (e.g.

promoter sequences) using known EMF sequences as a target sequence or motif, i.e. searching for upstream regulatory sequences by alignment with known promoter sequences. This process is a search function which merely scans an input sequence for target motifs. This process has nothing to do with reducing syngeneic redundancy in general, and does not and can not correlate the sequence identifiers of the first subset with syngeneic biopolymers to output a second subset of the dataset having reduced unique, natural complex biopolymer redundancy.

35USC103(a): Claim 5 and 7.

Claim 5 and 7 are each dependent on, and require all the limitations recited in claim 1. Claim 5 further requires that the recited dataset is GenBank, Medline or KEGG; and claim 7 further requires that the recited database is UniGene or LocusLink. As noted in the cited Chin et al. (US Pat. No. 6,470,277) and MacLeod et al. (US Pat. No. 6,221,600), these are well-known sequence databases, and which provide particularly suited datasets for use in our claimed methods. However, there is no prior art, Ford et al. (supra) or otherwise, teaching or suggesting our claimed methods, regardless of which recited datasets or databases are incorporated.

The Examiner is invited to call the undersigned if she would like to amend the claims to clarify the foregoing or seeks further clarification of the claim language.

We petition for and authorize charging our Deposit Account No.19-0750 all necessary extensions of time. The Commissioner is authorized to charge any fees or credit any overcharges relating to this communication to our Dep. Acct. No.19-0750 (order UTSD:0668).

Respectfully submitted,
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